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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/961,400

DATE: 08/05/2002
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3 <110> APPLICANT: RYBAK, SUSANNA M.
 4 GOLDENBERG, DAVID M.
 5 NEWTON, DIANNE L.
 7 <120> TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
 8 CELLS
 10 <130> FILE REFERENCE: 018733/1059
 12 <140> CURRENT APPLICATION NUMBER: 09/961,400
 13 <141> CURRENT FILING DATE: 2001-09-25
 15 <150> PRIOR APPLICATION NUMBER: 09/622,613
 16 <151> PRIOR FILING DATE: 2000-08-17
 18 <150> PRIOR APPLICATION NUMBER: PCT/US99/06641
 19 <151> PRIOR FILING DATE: 1999-03-26
 21 <150> PRIOR APPLICATION NUMBER: 60/079,751
 22 <151> PRIOR FILING DATE: 1998-03-26
 24 <160> NUMBER OF SEQ ID NOS: 43
 26 <170> SOFTWARE: PatentIn Ver. 2.1
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 30 <212> TYPE: DNA
 31 <213> ORGANISM: Rana pipiens
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 35 <222> LOCATION: (1)..(312)
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 40 1 5 10 15
 42 gtt gac tgt aat aat atc atg tca aca aac ttg ttc cac tgc aag gac 96
 43 Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys Asp
 44 20 25 30
 46 aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc tgt 144
 47 Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys
 48 35 40 45
 50 aaa gga att ata gcc tcc aaa aat gtg tta act acc tct gag ttt tat 192
 51 Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe Tyr
 52 50 55 60
 54 ctc tct gat tgc aat gta aca agc agg cct tgc aag tat aaa tta aag 240
 55 Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
 56 65 70 75 80
 58 aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca gta 288
 59 Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro Val
 60 85 90 95
 62 cat ttc gtg ggt gtc gga cat tgc 312

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69 <212> TYPE: PRT

70 <213> ORGANISM: Rana pipiens

72 <400> SEQUENCE: 2

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74 1 5 10 15

76 Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys Asp

77 20 25 30

79 Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys

80 35 40 45

82 Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe Tyr

83 50 55 60

85 Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys

86 65 70 75 80

88 Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro Val

89 85 90 95

91 His Phe Val Gly Val Gly His Cys

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99 <213> ORGANISM: Rana pipiens

101 <220> FEATURE:

102 <221> NAME/KEY: CDS

103 <222> LOCATION: (1)..(312)

105 <400> SEQUENCE: 3

106 caa gac tgg ctt acg ttt cag aag aag cac ctg aca aac acc cgg gat 48

107 Gln Asp Trp Leu Thr Phe Gln Lys Lys His Leu Thr Asn Thr Arg Asp

108 1 5 10 15

110 gtt gac tgt aat aat atc ctg tca aca aac ttg ttc cac tgc aag gac 96

111 Val Asp Cys Asn Asn Ile Leu Ser Thr Asn Leu Phe His Cys Lys Asp

112 20 25 30

114 aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc tgt 144

115 Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys

116 35 40 45

118 aaa gga att ata gcc tcc aaa aat gtg tta act acc ttt gag ttt tat 192

119 Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe Tyr

120 50 55 60

122 ctc tct gat tgc aat gta aca agc agg cct tgc aag tat aaa tta aag 240

123 Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys

124 65 70 75 80

126 aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca gta 288

127 Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro Val

128 85 90 95

130 cat ttc gtg ggt gtc gga cat tgc 312

131 His Phe Val Gly Val Gly His Cys

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144 Val Asp Cys Asn Asn Ile Leu Ser Thr Asn Leu Phe His Cys Lys Asp
145          20          25          30
147 Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys
148          35          40          45
150 Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe Tyr
151          50          55          60
153 Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
154   65          70          75          80
156 Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro Val
157          85          90          95
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165 <211> LENGTH: 315
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167 <213> ORGANISM: Rana pipiens
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171 <222> LOCATION: (1)..(315)
173 <400> SEQUENCE: 5
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176   1          5          10          15
178 gat gtt gac tgt aat aat atc atg tca aca aac ttg ttc cac tgc aag      96
179 Asp Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys
180          20          25          30
182 gac aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc      144
183 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
184          35          40          45
186 tgt aaa gga att ata gcc tcc aaa aat gtg tta act acc tct gag ttt      192
187 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe
188          50          55          60
190 tat ctc tct gat tgc aat gta aca agc agg cct tgc aag tat aaa tta      240
191 Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu
192   65          70          75          80
194 aag aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca      288
195 Lys Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro
196          85          90          95
198 gta cat ttc gtg ggt gtc gga cat tgc      315
199 Val His Phe Val Gly Val Gly His Cys
200          100          105

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205 <212> TYPE: PRT
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212 Asp Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys
213           20           25           30
215 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
216           35           40           45
218 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe
219           50           55           60
221 Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu
222  65           70           75           80
224 Lys Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro
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238 <221> NAME/KEY: CDS
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244   1           5           10           15
246 gat gtt gac tgt aat aat atc ctg tca aca aac ttg ttc cac tgc aag   96
247 Asp Val Asp Cys Asn Asn Ile Leu Ser Thr Asn Leu Phe His Cys Lys
248           20           25           30
250 gac aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc   144
251 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
252           35           40           45
254 tgt aaa gga att ata gcc tcc aaa aat gtg tta act acc ttt gag ttt   192
255 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe
256           50           55           60
258 tat ctc tct gat tgc aat gca aca agc agg cct tgc aag tat aaa tta   240
259 Tyr Leu Ser Asp Cys Asn Ala Thr Ser Arg Pro Cys Lys Tyr Lys Leu
260  65           70           75           80
262 aag aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca   288
263 Lys Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro
264           85           90           95
266 gta cat ttc gtg ggt gtc gga cat tgc   315
267 Val His Phe Val Gly Val Gly His Cys
268           100          105
271 <210> SEQ ID NO: 8

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281           20           25           30
283 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
284           35           40           45
286 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe
287           50           55           60
289 Tyr Leu Ser Asp Cys Asn Ala Thr Ser Arg Pro Cys Lys Tyr Lys Leu
290   65           70           75           80
292 Lys Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro
293           85           90           95
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296           100          105
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305 <400> SEQUENCE: 9
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310           20           25           30
312 Asn Leu Phe His Cys Lys Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro
313           35           40           45
315 Glu Pro Val Lys Ala Ile Cys Lys Gly Ile Ile Ala Ser Lys Asn Val
316           50           55           60
318 Leu Thr Thr Ser Glu Phe Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg
319   65           70           75           80
321 Pro Cys Lys Tyr Lys Leu Lys Lys Ser Thr Asn Thr Phe Cys Val Thr
322           85           90           95
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325           100          105          110
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335 <222> LOCATION: (1)..(312)
337 <400> SEQUENCE: 10
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339 Ser Asp Trp Leu Thr Phe Gln Lys Lys His Leu Thr Asn Thr Arg Asp
340   1           5           10           15
342 gtt gac tgt aat aat atc atg tca aca aac ttg ttc cac tgc aag gac   96

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